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SEQUENCE LISTING

*Pub
B3*

<110> Hauptmann, Rudolph
Himmler, Adolph
Maurer-Fogy, Ingrid
Stratowa, Christian

<120> TNF Receptors, TNF Binding Proteins and DNAs Coding for
Them

<130> 98,385-J

<140> 09/899,429

<141> 2001-07-03

<150> 09/792,356

<151> 2000-02-23

<150> 08/477,639

<151> 1955-06-07

<150> 08/383,676

<151> 1995-02-01

<150> 08/153,287

<151> 1993-11-17

<150> 07/821,750

<151> 1992-01-02

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<151> 1990-04-20

<160> 87

<170> PatentIn Ver. 2.0

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<222> (1)..(87)

<220>

<221> misc_feature

<222> (88)..(120)

<223> Portion of TNF-BP pro protein cleaved by
extracellular proteases following secretion.

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<222> (606)..(633)

<223> Portion of TNF-BP pro protein cleaved by extracellular proteases following secretion.

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gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct 96
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
20 25 30

cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa 144
His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
35 40 45

tat atc cac cct caa aat aat tgc att tgc tgt acc aag tgc cac aaa 192
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
50 55 60

gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac 240
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
65 70 75 80

tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc 288
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
85 90 95

aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg 336
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
100 105 110

gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg 384
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
115 120 125

aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc 432
Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
130 135 140

aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag 480
Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
145 150 155 160

aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa 528
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
165 170 175

aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg 576
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
180 185 190

aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca 624
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
195 200 205

ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt 672
 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
 210 215 220

tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag 720
 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
 225 230 235 240

tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag 768
 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
 245 250 255

ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc 816
 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
 260 265 270

ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg 864
 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
 275 280 285

ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt 912
 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
 290 295 300

ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg 960
 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
 305 310 315 320

gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac ccc atc ccc aac 1008
 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
 325 330 335

ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac 1056
 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
 340 345 350

act gat gac ccc gcg acg ctg tac gcc gtg gtg gag aac gtg ccc ccg 1104
 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
 355 360 365

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 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
 370 375 380

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 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
 385 390 395 400

tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc 1248
 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
 405 410 415

acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc 1296
 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
 420 425 430

tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg 1344
 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
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ccc gcg ccc agt ctt ctc aga tga 1368
 Pro Ala Pro Ser Leu Leu Arg
 450 455

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 <213> Homo sapiens

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 35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
 50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
 65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
 85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
 100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
 130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
 145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
 165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
 180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
 195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
 210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
245 250 255

Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
275 280 285

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
290 295 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
305 310 315 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
325 330 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
340 345 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
355 360 365

Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
370 375 380

Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
385 390 395 400

Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
405 410 415

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
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 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt 96
 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
 20 25 30
 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc 144
 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
 35 40 45
 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa 192
 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
 50 55 60
 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac 240
 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
 65 70 75 80
 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg 288
 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
 85 90 95
 agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg 336
 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
 100 105 110
 acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc 384
 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
 115 120 125
 cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac 432
 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
 130 135 140
 tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag 480
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 aat 483
 Asn

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 35 40 45

Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
 50 55 60
 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
 65 70 75 80
 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
 85 90 95
 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
 100 105 110
 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
 115 120 125
 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
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 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
 145 150 155 160
 Asn

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 <213> Homo sapiens

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 gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga 87
 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly
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 <212> PRT
 <213> Homo sapiens

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 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly
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<212> DNA
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<222> (1)..(33)

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1 5 10

33

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<212> PRT
<213> Homo sapiens

<400> 8
Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg
1 5 10

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<212> DNA
<213> Homo sapiens

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Val Lys Gly Thr Glu Asp Ser Gly Thr Thr
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30

<210> 10
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ctggacagac cgagtcccgg gaagccccag cactgccgct gccacactgc cctgagccca 180

aatgggacgag tgagaggcca tagctgtctg gc atg ggc ctc tcc acc gtg cct 233
Met Gly Leu Ser Thr Val Pro
1 5

gac ctg ctg ctg cca ctg ggc ctc ctg gag ctg ttg gtg gga ata tac 281
Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr
10 15 20

ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329
Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys
25 30 35

aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377
Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn
40 45 50 55

tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425
Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp
60 65 70

tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473
Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly
75 80 85

tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 521
Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser
90 95 100

aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 569
Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val
105 110 115

gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat 617
Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
120 125 130 135

tgg agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat 665
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn
140 145 150

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Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr
155 160 165

tgc cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt	761
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser	
170 175 180	
aac tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att	809
Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile	
185 190 195	
gag aat gtt aag ggc act gag gac tca ggc acc aca gtg ctg ttg ccc	857
Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro	
200 205 210 215	
ctg gtc att ttc ttt ggt ctt tgc ctt tta tcc ctc ctc ttc att ggt	905
Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly	
220 225 230	
tta atg tat cgc tac caa cgg tgg aag tcc aag ctc tac tcc att gtt	953
Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val	
235 240 245	
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Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr	
250 255 260	
act aag ccc ctg gcc cca aac cca agc ttc agt ccc act cca ggc ttc	1049
Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe	
265 270 275	
acc ccc acc ctg ggc ttc agt ccc gtg ccc agt tcc acc ttc acc tcc	1097
Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser	
280 285 290 295	
agc tcc acc tat acc ccc ggt gac tgt ccc aac ttt gcg gct ccc cgc	1145
Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg	
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aga gag gtg gca cca ccc tat cag ggg gct gac ccc atc ctt gcg aca	1193
Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr	
315 320 325	
gcc ctc gcc tcc gac ccc atc ccc aac ccc ctt cag aag tgg gag gac	1241
Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp	
330 335 340	
agc gcc cac aag cca cag agc cta gac act gat gac ccc gcg acg ctg	1289
Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu	
345 350 355	
tac gcc gtg gtg gag aac gtg ccc ccg ttg cgc tgg aaggaattc	1334
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360 365 370	

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 <212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: cDNA insert of
lambdaTNF-BP15 and pTNF-BP15 vectors

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His	Leu	Gly	Asp	Arg	Glu	Lys	Arg	Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys
		35					40					45			
Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile	Cys	Cys	Thr	Lys	Cys	His	Lys
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Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp
65					70				75						80
Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu
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Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val
			100					105					110		
Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg
		115					120					125			
Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe
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Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr
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Gly	Thr	Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	Gly	Leu	Cys	Leu
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Ser	Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys	Glu
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Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	Asn	Pro	Ser
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<210> 14

<211> 2173

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (245)..(1630)

<220>

<223> Description of Artificial Sequence: raTNF-R8

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gggctcacgc tgccaacacc cgggccacct ggtccgatcg tcttacttca ttcaccagcg 180

ttgccaattg ctgccctgtc cccagcccca atgggggagt gagagaggcc actgccggcc 240
 ggac atg ggt ctc ccc atc gtg cct ggc ctg ctg ctg tca ctg gtg ctc 289
 Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu
 1 5 10 15
 ctg gct ctg ctg atg ggg ata cac cca tca ggg gtc acc gga ctg gtt 337
 Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val
 20 25 30
 cct tct ctt ggt gac cgg gag aag agg gat aat ttg tgt ccc cag gga 385
 Pro Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly
 35 40 45
 aag tat gcc cat cca aag aat aat tcc atc tgc tgc acc aag tgc cac 433
 Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His
 50 55 60
 aaa gga acc tac ttg gtg agt gac tgt cca agc cca ggg cag gaa aca 481
 Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr
 65 70 75
 gtc tgc gag ctc tct cat aaa ggc acc ttt aca gct tgc cag aac cac 529
 Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His
 80 85 90 95
 gtc aga cag tgt ctc agt tgc aag aca tgt cgg aaa gaa atg ttc cag 577
 Val Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln
 100 105 110
 gtg gag att tct cct tgc aaa gct gac atg gac acc gtg tgt ggc tgc 625
 Val Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys
 115 120 125
 aag aag aac caa ttc cag cgc tac ctg agt gag acg cat ttc cag tgt 673
 Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys
 130 135 140
 gtg gac tgc agc ccc tgc ttc aat ggc acc gtg aca atc ccc tgt aag 721
 Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys
 145 150 155
 gag aaa cag aac acc gtg tgt aac tgc cac gca gga ttc ttt cta agc 769
 Glu Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser
 160 165 170 175
 gga aat gag tgc acc cct tgc agc cac tgc aag aaa aat cag gaa tgt 817
 Gly Asn Glu Cys Thr Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys
 180 185 190
 atg aag ctg tgc cta cct cca gtt gca aat gtc aca aac ccc cag gac 865
 Met Lys Leu Cys Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp
 195 200 205
 tca ggt act gcc gtg ctg ttg cct ctg gtt atc ttc cta ggt ctt tgc 913
 Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys

210						215						220						
ctt	tta	ttc	ttt	atc	tgc	atc	agt	cta	ctg	tgc	cga	tat	ccc	cag	tgg	961		
Leu	Leu	Phe	Phe	Ile	Cys	Ile	Ser	Leu	Leu	Cys	Arg	Tyr	Pro	Gln	Trp			
225						230						235						
agg	ccc	agg	gtc	tac	tcc	atc	att	tgt	agg	gat	tca	gct	cct	gtc	aaa	1009		
Arg	Pro	Arg	Val	Tyr	Ser	Ile	Ile	Cys	Arg	Asp	Ser	Ala	Pro	Val	Lys			
240				245				250				255						
gag	gtg	gag	ggg	gaa	gga	att	gtt	act	aag	ccc	cta	act	cca	gcc	tct	1057		
Glu	Val	Glu	Gly	Glu	Gly	Ile	Val	Thr	Lys	Pro	Leu	Thr	Pro	Ala	Ser			
			260						265			270						
atc	cca	gcc	ttc	agc	ccc	aac	ccc	ggc	ttc	aac	ccc	act	ctg	ggc	ttc	1105		
Ile	Pro	Ala	Phe	Ser	Pro	Asn	Pro	Gly	Phe	Asn	Pro	Thr	Leu	Gly	Phe			
275						280						285						
agc	acc	acc	cca	cgc	ttc	agt	cat	cct	gtc	tcc	agt	acc	ccc	atc	agc	1153		
Ser	Thr	Thr	Pro	Arg	Phe	Ser	His	Pro	Val	Ser	Ser	Thr	Pro	Ile	Ser			
290						295						300						
ccc	gtc	ttc	ggg	cct	agt	aac	tgg	cac	aac	ttc	gtg	cca	cct	gta	aga	1201		
Pro	Val	Phe	Gly	Pro	Ser	Asn	Trp	His	Asn	Phe	Val	Pro	Pro	Val	Arg			
305				310				315										
gag	gtg	gtc	cca	acc	cag	ggg	gct	gac	cct	ctc	ctc	tac	gga	tcc	ctc	1249		
Glu	Val	Val	Pro	Thr	Gln	Gly	Ala	Asp	Pro	Leu	Leu	Tyr	Gly	Ser	Leu			
320				325				330				335						
aac	cct	gtg	cca	atc	ccc	gcc	cct	gtt	cgg	aaa	tgg	gaa	gac	gtc	gtc	1297		
Asn	Pro	Val	Pro	Ile	Pro	Ala	Pro	Val	Arg	Lys	Trp	Glu	Asp	Val	Val			
			340						345			350						
gcg	gcc	cag	cca	caa	cgg	ctt	gac	act	gca	gac	cct	gcg	atg	ctg	tat	1345		
Ala	Ala	Gln	Pro	Gln	Arg	Leu	Asp	Thr	Ala	Asp	Pro	Ala	Met	Leu	Tyr			
355						360						365						
gct	gtg	gtg	gat	ggc	gtg	cct	ccg	aca	cgc	tgg	aag	gag	ttc	atg	cgg	1393		
Ala	Val	Val	Asp	Gly	Val	Pro	Pro	Thr	Arg	Trp	Lys	Glu	Phe	Met	Arg			
370						375						380						
ctc	ctg	ggg	ctg	agc	gag	cac	gag	atc	gag	cgg	ttg	gag	ctg	cag	aac	1441		
Leu	Leu	Gly	Leu	Ser	Glu	His	Glu	Ile	Glu	Arg	Leu	Glu	Leu	Gln	Asn			
385				390				395										
ggg	cgt	tgc	ctc	cgc	gag	gct	cat	tac	agc	atg	ctg	gaa	gcc	tgg	cgg	1489		
Gly	Arg	Cys	Leu	Arg	Glu	Ala	His	Tyr	Ser	Met	Leu	Glu	Ala	Trp	Arg			
400				405				410				415						
cgc	cgc	aca	ccg	cga	cac	gag	gcc	acg	ctg	gac	gta	gtg	ggc	cgc	gtg	1537		
Arg	Arg	Thr	Pro	Arg	His	Glu	Ala	Thr	Leu	Asp	Val	Val	Gly	Arg	Val			
			420						425			430						
ctt	tgc	gac	atg	aac	ctg	cgt	ggc	tgc	ctg	gag	aac	atc	cgc	gag	act	1585		
Leu	Cys	Asp	Met	Asn	Leu	Arg	Gly	Cys	Leu	Glu	Asn	Ile	Arg	Glu	Thr			
435						440						445						

cta gaa agc cct gcc cac tcg tcc acg acc cac ctc ccg cga taa 1630
 Leu Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro Arg
 450 455 460

ggccacaccc ccacctcagg aacgggactc gaaggaccat cctgctagat gccctgcttc 1690
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 ttc 2173

<210> 15
 <211> 461
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: raTNF-R8

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 Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro
 20 25 30
 Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly Lys
 35 40 45
 Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
 50 55 60
 Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val
 65 70 75 80
 Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val
 85 90 95
 Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val
 100 105 110
 Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys Lys

115					120					125					
Lys	Asn	Gln	Phe	Gln	Arg	Tyr	Leu	Ser	Glu	Thr	His	Phe	Gln	Cys	Val
130						135					140				
Asp	Cys	Ser	Pro	Cys	Phe	Asn	Gly	Thr	Val	Thr	Ile	Pro	Cys	Lys	Glu
145					150					155					160
Lys	Gln	Asn	Thr	Val	Cys	Asn	Cys	His	Ala	Gly	Phe	Phe	Leu	Ser	Gly
				165					170					175	
Asn	Glu	Cys	Thr	Pro	Cys	Ser	His	Cys	Lys	Lys	Asn	Gln	Glu	Cys	Met
			180					185					190		
Lys	Leu	Cys	Leu	Pro	Pro	Val	Ala	Asn	Val	Thr	Asn	Pro	Gln	Asp	Ser
	195						200					205			
Gly	Thr	Ala	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Leu	Gly	Leu	Cys	Leu
	210					215					220				
Leu	Phe	Phe	Ile	Cys	Ile	Ser	Leu	Leu	Cys	Arg	Tyr	Pro	Gln	Trp	Arg
225					230					235					240
Pro	Arg	Val	Tyr	Ser	Ile	Ile	Cys	Arg	Asp	Ser	Ala	Pro	Val	Lys	Glu
				245					250					255	
Val	Glu	Gly	Glu	Gly	Ile	Val	Thr	Lys	Pro	Leu	Thr	Pro	Ala	Ser	Ile
			260					265					270		
Pro	Ala	Phe	Ser	Pro	Asn	Pro	Gly	Phe	Asn	Pro	Thr	Leu	Gly	Phe	Ser
		275					280					285			
Thr	Thr	Pro	Arg	Phe	Ser	His	Pro	Val	Ser	Ser	Thr	Pro	Ile	Ser	Pro
	290					295					300				
Val	Phe	Gly	Pro	Ser	Asn	Trp	His	Asn	Phe	Val	Pro	Pro	Val	Arg	Glu
305					310					315					320
Val	Val	Pro	Thr	Gln	Gly	Ala	Asp	Pro	Leu	Leu	Tyr	Gly	Ser	Leu	Asn
				325					330					335	
Pro	Val	Pro	Ile	Pro	Ala	Pro	Val	Arg	Lys	Trp	Glu	Asp	Val	Val	Ala
			340					345					350		
Ala	Gln	Pro	Gln	Arg	Leu	Asp	Thr	Ala	Asp	Pro	Ala	Met	Leu	Tyr	Ala
		355					360					365			
Val	Val	Asp	Gly	Val	Pro	Pro	Thr	Arg	Trp	Lys	Glu	Phe	Met	Arg	Leu
	370					375					380				
Leu	Gly	Leu	Ser	Glu	His	Glu	Ile	Glu	Arg	Leu	Glu	Leu	Gln	Asn	Gly
385					390					395					400
Arg	Cys	Leu	Arg	Glu	Ala	His	Tyr	Ser	Met	Leu	Glu	Ala	Trp	Arg	Arg
				405					410					415	
Arg	Thr	Pro	Arg	His	Glu	Ala	Thr	Leu	Asp	Val	Val	Gly	Arg	Val	Leu

420	425	430
Cys Asp Met Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu		
435	440	445
Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro Arg		
450	455	460

<210> 16
 <211> 2141
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (213)..(1580)

<220>
 <223> Description of Artificial Sequence: human TNF-R in
 1TNF-R2

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 ctggacagac cgagtcccgg gaagccccag cactgccgct gccacactgc cctgagccca 180
 katgggggag tgagaggcca tagctgtctg gc atg ggc ctc tcc acc gtg cct 233
 Met Gly Leu Ser Thr Val Pro
 1 5
 gac ctg ctg ctg cca ctg gtg ctc ctg gag ctg ttg gtg gga ata tac 281
 Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr
 10 15 20
 ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329
 Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys
 25 30 35
 aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377
 Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn
 40 45 50 55
 tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425
 Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp
 60 65 70
 tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473
 Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly
 75 80 85
 tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 521
 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser
 90 95 100

aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg	569
Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val	
105 110 115	
gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat	617
Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr	
120 125 130 135	
tgg agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat	665
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn	
140 145 150	
ggg acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc	713
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr	
155 160 165	
tgc cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt	761
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser	
170 175 180	
aac tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att	809
Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile	
185 190 195	
gag aat gtt aag ggc act gag gac tca ggc acc aca gtg ctg ttg ccc	857
Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro	
200 205 210 215	
ctg gtc att ttc ttt ggt ctt tgc ctt tta tcc ctc ctc ttc att ggt	905
Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly	
220 225 230	
tta atg tat cgc tac caa cgg tgg aag tcc aag ctc tac tcc att gtt	953
Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val	
235 240 245	
tgt ggg aaa tcg aca cct gaa aaa gag ggg gag ctt gaa gga act act	1001
Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr	
250 255 260	
act aag ccc ctg gcc cca aac cca agc ttc agt ccc act cca ggc ttc	1049
Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe	
265 270 275	
acc ccc acc ctg ggc ttc agt ccc gtg ccc agt tcc acc ttc acc tcc	1097
Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser	
280 285 290 295	
agc tcc acc tat acc ccc ggt gac tgt ccc aac ttt gcg gct ccc cgc	1145
Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg	
300 305 310	
aga gag gtg gca cca ccc tat cag ggg gct gac ccc atc ctt gcg aca	1193
Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr	
315 320 325	
gcc ctc gcc tcc gac ccc atc ccc aac ccc ctt cag aag tgg gag gac	1241

Ala	Leu	Ala	Ser	Asp	Pro	Ile	Pro	Asn	Pro	Leu	Gln	Lys	Trp	Glu	Asp		
		330					335					340					
agc	gcc	cac	aag	cca	cag	agc	cta	gac	act	gat	gac	ccc	gcg	acg	ctg	1289	
Ser	Ala	His	Lys	Pro	Gln	Ser	Leu	Asp	Thr	Asp	Asp	Pro	Ala	Thr	Leu		
		345				350					355						
tac	gcc	gtg	gtg	gag	aac	gtg	ccc	ccg	ttg	cg	tgg	aag	gaa	ttc	gtg	1337	
Tyr	Ala	Val	Val	Glu	Asn	Val	Pro	Pro	Leu	Arg	Trp	Lys	Glu	Phe	Val		
		360			365				370					375			
cgg	cg	cta	ggg	ctg	agc	gac	cac	gag	atc	gat	cgg	ctg	gag	ctg	cag	1385	
Arg	Arg	Leu	Gly	Leu	Ser	Asp	His	Glu	Ile	Asp	Arg	Leu	Glu	Leu	Gln		
				380					385					390			
aac	ggg	cg	tgc	ctg	cg	gag	gcg	caa	tac	agc	atg	ctg	gcg	acc	tgg	1433	
Asn	Gly	Arg	Cys	Leu	Arg	Glu	Ala	Gln	Tyr	Ser	Met	Leu	Ala	Thr	Trp		
			395					400					405				
agg	cgg	cg	acg	ccg	cgg	cg	gag	gcc	acg	ctg	gag	ctg	ctg	gga	cg	1481	
Arg	Arg	Arg	Thr	Pro	Arg	Arg	Glu	Ala	Thr	Leu	Glu	Leu	Leu	Gly	Arg		
			410				415					420					
gtg	ctc	cg	gac	atg	gac	ctg	ctg	ggc	tgc	ctg	gag	gac	atc	gag	gag	1529	
Val	Leu	Arg	Asp	Met	Asp	Leu	Leu	Gly	Cys	Leu	Glu	Asp	Ile	Glu	Glu		
			425			430				435							
gcg	ctt	tgc	ggc	ccc	gcc	gcc	ctc	ccg	ccc	gcg	ccc	agt	ctt	ctc	aga	1577	
Ala	Leu	Cys	Gly	Pro	Ala	Ala	Leu	Pro	Pro	Ala	Pro	Ser	Leu	Leu	Arg		
			440			445				450				455			
tga	ggctgcgccc	ctgcgggcag	ctctaaggac	cgctcctgcga	gatcgccttc											1630	
caacccccact	tttttctgga	aaggaggggt	cctgcagggg	caagcaggag	ctagcagccg											1690	
cctaacttgg	gctaaccct	cgatgtacat	agcttttctc	agctgcctgc	gcgccgccga											1750	
cagtcagcgc	tgtgcgcgcg	gagagaggtg	cgccgtgggc	tcaagagcct	gagtgggtgg											1810	
tttgcgagga	tgagggacgc	tatgcctcat	gcccgttttg	gggtgcctca	ccagcaaggc											1870	
tgtcggggg	cccctgggtc	gtccctgagc	ctttttcaca	gtgcataagc	agtttttttt											1930	
gtttttgttt	tgttttgttt	tgtttttaaa	tcaatcatgt	tacactaata	gaaacttggc											1990	
actcctgtgc	cctctgcctg	gacaagcaca	tagcaagctg	aactgtccta	aggcaggggc											2050	
gagcacggaa	caatggggcc	ttcagctgga	gctgtggact	tttgtacata	cactaaaatt											2110	
ctgaagttaa	aaaaaaaaaa	aaaaggaatt	c													2141	

<210> 17

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: human TNF-R in
1TNF-R2

<400> 17

Met	Gly	Leu	Ser	Thr	Val	Pro	Asp	Leu	Leu	Leu	Pro	Leu	Val	Leu	Leu	
1				5				10						15		
Glu	Leu	Leu	Val	Gly	Ile	Tyr	Pro	Ser	Gly	Val	Ile	Gly	Leu	Val	Pro	
			20					25					30			
His	Leu	Gly	Asp	Arg	Glu	Lys	Arg	Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	
		35					40					45				
Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	
	50					55					60					
Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	
	65				70					75					80	
Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	
				85					90					95		
Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	
			100					105					110			
Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	
		115					120					125				
Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	
	130					135					140					
Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	
	145				150					155					160	
Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	
				165					170					175		
Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	
			180					185					190			
Lys	Leu	Cys	Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	Thr	Glu	Asp	Ser	
		195					200					205				
Gly	Thr	Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	Gly	Leu	Cys	Leu	
	210					215					220					
Leu	Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	Gln	Arg	Trp	Lys	
	225				230					235					240	
Ser	Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys	Glu	
				245					250					255		
Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	Asn	Pro	Ser	
			260					265					270			

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
 275 280 285
 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
 290 295 300
 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
 305 310 315 320
 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
 325 330 335
 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
 340 345 350
 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
 355 360 365
 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
 370 375 380
 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
 385 390 395 400
 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
 405 410 415
 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
 420 425 430
 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
 435 440 445
 Pro Ala Pro Ser Leu Leu Arg
 450 455

<210> 18
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: N-terminal
 amino acid sequence of protein purified from urine
 (main sequence)

<220>
 <221> UNSURE
 <222> (4)
 <223> Identity of "Xaa" could not be determined.

<400> 18
 Asp Ser Val Xaa Pro Gln Gly Lys Tyr Ile His Pro Gln
 1 5 10

<210> 19
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: N-terminal
amino acid sequence of protein purified from urine
(sudsidiary sequence)

<220>
<221> UNSURE
<222> (7)
<223> Identity of "Xaa" could not be determined.

<400> 19
Leu Val Pro His Leu Gly Xaa Arg Glu
1 5

<210> 20
<211> 151
<212> DNA
<213> Homo sapiens

<400> 20
caggggaaaa tattcaccct caaataattc gatttgctgt accaagtgcc acaaaggaaa 60
ctacttgtag aatgactgtc caggcccggg gcaggatagc gactgcaggg agtgtgagag 120
cggtccttc acagcctcag aaaacaacaa g 151

<210> 21
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 21
Asp Ser Val Cys Pro Gln Gly Lys
1 5

<210> 22
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<220>

<221> UNSURE
 <222> (1)..(2)
 <223> Identity of "Xaa" could not be determined.

<400> 22
 Xaa Xaa Leu Ser Cys Ser Lys
 1 5

<210> 23
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: TNF-BP tryptic
 cleavage peptide

<400> 23
 Asp Thr Val Cys Gly Cys Arg
 1 5

<210> 24
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: TNF-BP tryptic
 cleavage peptide

<400> 24
 Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys
 1 5 10

<210> 25
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: TNF-BP tryptic
 cleavage peptide

<400> 25
 Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys
 1 5 10

<210> 26
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<220>

<221> UNSURE

<222> (6)

<223> Identity of "Xaa" could not be determined.

<220>

<221> UNSURE

<222> (10)..(12)

<223> Identity of "Xaa" could not be determined.

<400> 26

Tyr Ile His Pro Gln Xaa Asn Ser Ile Xaa Xaa Xaa Lys
1 5 10

<210> 27

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 27

Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys
1 5 10

<210> 28

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 28

Leu Val Pro His Leu Gly Asp Arg
1 5

<210> 29

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 29

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg

1

5

10

15

<210> 30

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 30

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln

1

5

10

<210> 31

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<220>

<221> UNSURE

<222> (9)..(11)

<223> Identity of "Xaa" could not be determined.

<400> 31

Glu Met Gly Gln Val Glu Ile Ser Xaa Xaa Xaa Val Asp

1

5

10

<210> 32

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 32

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp

1

5

10

15

Thr Val Cys Gly

20

<210> 33

<211> 19

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<220>
<221> UNSURE
<222> (6)
<223> Identity of "Xaa" could not be determined.

<220>
<221> UNSURE
<222> (18)
<223> Identity of "Xaa" could not be determined.

<400> 33
Tyr Ile His Pro Gln Xaa Asn Ser Ile Cys Cys Thr Lys Cys His Lys
1 5 10 15

Gly Xaa Tyr

<210> 34
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<220>
<221> UNSURE
<222> (16)..(17)
<223> Identity of "Xaa" could not be determined.

<400> 34
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Xaa
1 5 10 15

Xaa Arg

<210> 35
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 35
Leu Cys Leu Pro Gln Ile Glu Asn
1 5

<210> 36
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: TNF-BP tryptic
 cleavage peptide

 <220>
 <221> UNSURE
 <222> (7)
 <223> Identity of "Xaa" could not be determined.

 <400> 36
 Gln Asn Thr Val Cys Thr Xaa His Ala Gly Phe Phe Leu Arg
 1 5 10

 <210> 37
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: TNF-BP tryptic
 cleavage peptide

 <400> 37
 Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn
 1 5 10

 <210> 38
 <211> 13
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> Description of Artificial Sequence: TNF-BP tryptic
 cleavage peptide

 <400> 38
 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln
 1 5 10

 <210> 39
 <211> 7
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> Description of Artificial Sequence: TNF-BP tryptic
 cleavage peptide

<400> 39
Gln Gly Lys Tyr Ile His Pro
1 5

<210> 40
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 40
caaggtaa atattcatcc 20

<210> 41
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 41
cagggtaa gt acatccatcc 20

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 42
caaggtaa atatacatcc 20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 43
caaggcaa atattcatcc 20

<210> 44
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 44
 cagggcaagt acatccaccc 20

 <210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 45
 caaggcaa atatacatcc 20

 <210> 46
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 46
 caaggaaa atattcatcc 20

 <210> 47
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 47
 cagggaaagt acatccaccc 20

 <210> 48
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hybridization probe

<400> 48
 caaggaaaat atatacatcc 20

<210> 49
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hybridization probe

<400> 49
 caagggaaat atattcatcc 20

<210> 50
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hybridization probe

<400> 50
 caggggaagt acatccaccc 20

<210> 51
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hybridization probe

<400> 51
 caagggaaat atatacatcc 20

<210> 52
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 52
Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys
1 5 10

<210> 53
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 53
Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Cys Asn Asn Lys
1 5 10

<210> 54
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 54
Phe Thr Ala Ser Glu Asn Asn Lys
1 5

<210> 55
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 55
Phe Thr Ala Ser Cys Asn Asn Lys
1 5

<210> 56
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 56

aaatgacgga gactcttggt gttcctaggg

30

<210> 57

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization
probe

<400> 57

aagtggcgta gtcttttggt gttcctaggg

30

<210> 58

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization
probe

<400> 58

aaatgtcgga gactcttggt gttcctaggg

30

<210> 59

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization
probe

<400> 59

aaatgacggt cactcttggt gttcctaggg

30

<210> 60

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization
probe

<400> 60

aagtggcggt ctcttttggt gttcctaggg

30

<210> 61

<211> 30

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 61
 aaatgtcggg cactcttggt gttcctaggg 30

 <210> 62
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 62
 aaatgacgga gaacattggt gttcctaggg 30

 <210> 63
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 63
 aagtggcgta gtactttggt gttcctaggg 30

 <210> 64
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 64
 aaatgtcggg gaacattggt gttcctaggg 30

 <210> 65
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization

probe

<400> 65
aaatgacggt caacattggt gttcctaggg 30

<210> 66
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 66
aagtggcggt ctactttggt gttcctaggg 30

<210> 67
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 67
aaatgtcggt caacattggt gttcctaggg 30

<210> 68
<211> 158
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(153)

<400> 68
cag ggg aaa tat att cac cct caa aat aat tcg att tgc tgt acc aag 48
Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys
1 5 10 15

tgc cac aaa gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag 96
Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln
20 25 30

gat acg gac tgc agg gag tgt gag agc ggc tcc ttc aca gcc tca gaa 144
Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu
35 40 45

aac aac aag gatcc 158
Asn Asn Lys
50

<210> 69
<211> 51
<212> PRT
<213> Homo sapiens

<400> 69
Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys
1 5 10 15
Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln
20 25 30
Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu
35 40 45
Asn Asn Lys
50

<210> 70
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
EBI-1786

<400> 70
ggaattcagc ctgaatggcg aatggg

26

<210> 71
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
EBI-1729

<400> 71
cctcgagcgt tgctggcggt tttcc

25

<210> 72
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
EBI-1733

<400> 72

ggtcgacatt gattattgac tag

23

<210> 73

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer
EBI-1734

<400> 73

ggaattccct aggaatacag cgg

23

<210> 74

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutagenesis
primer EBI-1751

<400> 74

gtacttgaac tcgttcctg

19

<210> 75

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutagenesis
primer EBI-1857

<400> 75

ggcaagggca gcagccgg

18

<210> 76

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide EBI-1823

<400> 76

agcttctgca ggtcgacatc gatggatcgg tacctcgagc ggccgcgaat tct

53

<210> 77

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide EBI-1829

<400> 77

ctagagaatt cgcggccgct cgaggtagcg gatccatcga tgcgacctg caga 54

<210> 78

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide EBI-1820

<400> 78

agctctagag attcgcggcc gtcgaggtta ccggatccat cgatgtcgac ctgcagaagc 60

ttg

63

<210> 79

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide EBI-1821

<400> 79

ctagcaagct tctgcaggtc gacatcgatg gatccggtag ctcgagcggc cgcgaattct 60

ctag

64

<210> 80

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer
EBI-1986

<400> 80

caggatccga gtctcaaccc tcaac

25

<210> 81

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer
EBI-1929

<400> 81

gggaattcct tatcaattct caatctgggg taggcacaac ttc

43

<210> 82

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer
EBI-2452

<400> 82

cacagtcgac ttacatttgc ttctgacaca actgtgttca ctagcaacct caaacagaca 60

ccatgggcct ctccaccgtg c

81

<210> 83

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer
EBI-1922

<400> 83

gaggctgcaa ttgaagc

17

<210> 84

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer
EBI-2316

<400> 84

attcgtgcgg cgcctag

17

<210> 85

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer
EBI-2467

<400> 85
gtcggtagca ccaagga

17

<210> 86
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
EBI-1986

<400> 86
gttttcccag tcacgac

17

<210> 87
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Sequencing
primer EBI-2112

<400> 87
gtccaattat gtcacacc

18